

## Alignments

>emb|V00866.1|HBVADW Hepatitis B virus complete DNA sequence (subtype adw)  
Length=3200

Score = 5906 bits (3198), Expect = 0.0  
Identities = 3198/3198 (100%), Gaps = 0/3198 (0%)  
Strand=Plus/Plus

Query	3	TTCCACTGCCTTGCACCAAGCTCTGCAGGATCCCAGAGTCAGGGCTGTATCTCCTGC	62
Sbjct	1	TTCCACTGCCTTGCACCAAGCTCTGCAGGATCCCAGAGTCAGGGCTGTATCTCCTGC	60
Query	63	TGGTGGCTCAGTCAGGAACAGTAAACCCCTGCCAATTGCGCTCACATCTCGTC	122
Sbjct	61	TGGTGGCTCAGTCAGGAACAGTAAACCCCTGCCAATTGCGCTCACATCTCGTC	120
Query	123	AATCTCCGCGAGGACTGGGGACCTGTGACGATCATGGAGAACATCACATCAGGATTCT	182
Sbjct	121	AATCTCCGCGAGGACTGGGGACCTGTGACGATCATGGAGAACATCACATCAGGATTCT	180
Query	183	AGGACCCCTGCTCGTGTACAGGCGGGTTTCTTGTGACAAGAACATCCTCACAAATACC	242
Sbjct	181	AGGACCCCTGCTCGTGTACAGGCGGGTTTCTTGTGACAAGAACATCCTCACAAATACC	240
Query	243	GCAGAGTCTAGACTCGTGGACTTCTCAATTCTAGGGGATCACCCGTGTGTCT	302
Sbjct	241	GCAGAGTCTAGACTCGTGGACTTCTCAATTCTAGGGGATCACCCGTGTGTCT	300
Query	303	TGGCCAAAATTGCGAGTCCCCAACCTCCAATCACTCACCAACCTCCTGTCCTCCAATTG	362
Sbjct	301	TGGCCAAAATTGCGAGTCCCCAACCTCCAATCACTCACCAACCTCCTGTCCTCCAATTG	360
Query	363	TCCTGGTTATCGCTGGATGTCTGCGGCCTTATCATATTCTCATCCTGCTGCT	422
Sbjct	361	TCCTGGTTATCGCTGGATGTCTGCGGCCTTATCATATTCTCATCCTGCTGCT	420
Query	423	ATGCCTCATCTTATTGGTCTCTGGATTATCAAGGTATGTTGCCGTTGTCCTCT	482
Sbjct	421	ATGCCTCATCTTATTGGTCTCTGGATTATCAAGGTATGTTGCCGTTGTCCTCT	480
Query	483	AATTCCAGGATCAACAACACCAGTACGGGACCATGCAAAACCTGCACGACTCCTGCTCA	542
Sbjct	481	AATTCCAGGATCAACAACACCAGTACGGGACCATGCAAAACCTGCACGACTCCTGCTCA	540
Query	543	AGGCAACTTAAGTTCCCTCATGTTGCTGTACAAAACCTACGGATGGAAATTGCACCTG	602
Sbjct	541	AGGCAACTTAAGTTCCCTCATGTTGCTGTACAAAACCTACGGATGGAAATTGCACCTG	600
Query	603	TATTCCCATCCCATCGTCCCTGGGCTTCGCAAAATACCTATGGGAGTGGGCTCAGTCCG	662
Sbjct	601	TATTCCCATCCCATCGTCCCTGGGCTTCGCAAAATACCTATGGGAGTGGGCTCAGTCCG	660
Query	663	TTTCTCTGGCTCAGTTACTAGTGCCTTGTGAGTGGGCTTCCCCAC	722
Sbjct	661	TTTCTCTGGCTCAGTTACTAGTGCCTTGTGAGTGGGCTTCCCCAC	720
Query	723	TGTTGGCTTCAGCTATATGGATGATGTGGTATTGGGGCCAAGTCTGTACAGCATCGT	782
Sbjct	721	TGTTGGCTTCAGCTATATGGATGATGTGGTATTGGGGCCAAGTCTGTACAGCATCGT	780
Query	783	GAGTCCCTTATACCGCTGTTACCAATTCTTGTCTGGTATACATTAAACCT	842
Sbjct	781	GAGTCCCTTATACCGCTGTTACCAATTCTTGTCTGGTATACATTAAACCT	840
Query	843	AACAAAACAAAAAGATGGGTTATCCCTAAACTCATGGCTACATAATTGGAAGTTGG	902
Sbjct	841	AACAAAACAAAAAGATGGGTTATCCCTAAACTCATGGCTACATAATTGGAAGTTGG	900
Query	903	GGAACCTTGCCACAGGATCATATTGTACAAAAGATCAAACACTGTTAGAAAACCTCCT	962
Sbjct	901	GGAACCTTGCCACAGGATCATATTGTACAAAAGATCAAACACTGTTAGAAAACCTCCT	960
Query	963	GTAAACAGGCCTATTGATTGAAAGTATGTCAAAGAATTGTGGCTTTGGCTTGCT	1022
Sbjct	961	GTAAACAGGCCTATTGATTGAAAGTATGTCAAAGAATTGTGGCTTTGGCTTGCT	1020
Query	1023	GCTCCATTACACAATGTGGATATCCTGCCTTAATGCCTTGTATGCATGTACAGCT	1082
Sbjct	1021	GCTCCATTACACAATGTGGATATCCTGCCTTAATGCCTTGTATGCATGTACAGCT	1080

Query	1083	AAACAGGCTTCACTTCTGCCAACTTACAAGGCCTTCTAAGTAAACAGTACATGAAC 	1142
Sbjct	1081	AAACAGGCTTCACTTCTGCCAACTTACAAGGCCTTCTAAGTAAACAGTACATGAAC 	1140
Query	1143	CTTACCCCGTTGCTCGCAACGGCCTGGCTGTGCCAAGTGTGCTGACGCCAACCCCC 	1202
Sbjct	1141	CTTACCCCGTTGCTCGCAACGGCCTGGCTGTGCCAAGTGTGCTGACGCCAACCCCC 	1200
Query	1203	ACTGGCTGGGGCTTAGGCATAGGCCATCAGCGATGCGTGGAACCTTGTGGCTCCTCTG 	1262
Sbjct	1201	ACTGGCTGGGGCTTAGGCATAGGCCATCAGCGATGCGTGGAACCTTGTGGCTCCTCTG 	1260
Query	1263	CCGATCCATACTGCGGAACCTCTAGCCGCTGTTGCTCGCAGCCGGCTGGAGCAAAG 	1322
Sbjct	1261	CCGATCCATACTGCGGAACCTCTAGCCGCTGTTGCTCGCAGCCGGCTGGAGCAAAG 	1320
Query	1323	CTCATCGGAACTGACAATTCTGTCGTCCTCTCGCGAAATATACATCATTTCCATGGCTG 	1382
Sbjct	1321	CTCATCGGAACTGACAATTCTGTCGTCCTCTCGCGAAATATACATCATTTCCATGGCTG 	1380
Query	1383	CTAGGCTGACTGCCAAGTGGATCCTCGCGGGACGTCTTGTACGTCCCCTCGCG 	1442
Sbjct	1381	CTAGGCTGACTGCCAAGTGGATCCTCGCGGGACGTCTTGTACGTCCCCTCGCG 	1440
Query	1443	CTGAATCCCGCGGACGACCCCTCTCGGGGCGCTGGGACTCTCTCGTCCCCCTCTCCGT 	1502
Sbjct	1441	CTGAATCCCGCGGACGACCCCTCTCGGGGCGCTGGGACTCTCTCGTCCCCCTCTCCGT 	1500
Query	1503	CTGCCGTTCCAGCCGACCACGGGCGCACCTCTTACCGGCTCCCCGTCTGTGCCT 	1562
Sbjct	1501	CTGCCGTTCCAGCCGACCACGGGCGCACCTCTTACCGGCTCCCCGTCTGTGCCT 	1560
Query	1563	TCTCATCTGCCGGTCCGTGTGCACTTCGCTCACCTCTGCACGTTGCATGGGACCAACCG 	1622
Sbjct	1561	TCTCATCTGCCGGTCCGTGTGCACTTCGCTCACCTCTGCACGTTGCATGGGACCAACCG 	1620
Query	1623	TGAACGCCCATCAGATCCTGCCAAGGTCTTACATAAGAGGACTCTGGACTCCCAGCAA 	1682
Sbjct	1621	TGAACGCCCATCAGATCCTGCCAAGGTCTTACATAAGAGGACTCTGGACTCCCAGCAA 	1680
Query	1683	TGTCAACGACCGACCTTGAGGCCTACTTCAAAGACTGTGTGTTAAGGACTGGAGGAGT 	1742
Sbjct	1681	TGTCAACGACCGACCTTGAGGCCTACTTCAAAGACTGTGTGTTAAGGACTGGAGGAGT 	1740
Query	1743	TGGGGGAGGAGATTAGTTAATGATCTTGATTAGGAGGCTGTAGGCATAAATTGGTCT 	1802
Sbjct	1741	TGGGGGAGGAGATTAGTTAATGATCTTGATTAGGAGGCTGTAGGCATAAATTGGTCT 	1800
Query	1803	GCGCACCAAGACCATGCAACTTTCACCTCTGCCATAATCATCTTGTACATGTCCCAC 	1862
Sbjct	1801	GCGCACCAAGACCATGCAACTTTCACCTCTGCCATAATCATCTTGTACATGTCCCAC 	1860
Query	1863	TGTTCAAGCCTCCAAGCTGTGCCTGGTGGCTTGGGCATGGACATTGACCCCTATAA 	1922
Sbjct	1861	TGTTCAAGCCTCCAAGCTGTGCCTGGTGGCTTGGGCATGGACATTGACCCCTATAA 	1920
Query	1923	AGAATTGGAGCTACTGTGGAGTTACTCTCGTTTGCCTCTGACTTCTTCCTCCGT 	1982
Sbjct	1921	AGAATTGGAGCTACTGTGGAGTTACTCTCGTTTGCCTCTGACTTCTTCCTCCGT 	1980
Query	1983	ACGAGATCTCTAGACACCGCCTCAGCTCTGTATCGAGAACGCCTAGAGTCCTGAGCA 	2042
Sbjct	1981	ACGAGATCTCTAGACACCGCCTCAGCTCTGTATCGAGAACGCCTAGAGTCCTGAGCA 	2040
Query	2043	TTGCTCACCTCACCATACTGCACTCAGGCAAGCCATTCTCTGCTGGGGGAATTGATGAC 	2102
Sbjct	2041	TTGCTCACCTCACCATACTGCACTCAGGCAAGCCATTCTCTGCTGGGGGAATTGATGAC 	2100
Query	2103	TCTAGCTACCTGGTGGTAATAATTGCAAGATCCAGCATCCAGAGATCTAGTAGTCAA 	2162
Sbjct	2101	TCTAGCTACCTGGTGGTAATAATTGCAAGATCCAGCATCCAGAGATCTAGTAGTCAA 	2160
Query	2163	TTATGTTAATACATGGTTAAAGATCAGGCAACTATTGTGGTTCATATATCTG 	2222
Sbjct	2161	TTATGTTAATACATGGTTAAAGATCAGGCAACTATTGTGGTTCATATATCTG 	2220
Query	2223	CCTTACTTTGGAAGAGAGACTGTACTGAAATTGCTCTTCGGAGTGTGGATTG 	2282
Sbjct	2221	CCTTACTTTGGAAGAGAGACTGTACTGAAATTGCTCTTCGGAGTGTGGATTG 	2280
Query	2283	CACTCCTCCAGCCTATAGACCACCAATGCCCTATCTTATCAACACTTCCGGAAACTAC 	2342

Sbjct	2281	CACTCCTCCAGCCTATAGACCACCAAATGCCCTATCTTATCACACACTCCGGAAACTAC	2340
Query	2343	TGTTGTTAGACGACGGGACCGAGGCAGGTCCCCTAGAAGAAGAACCTCCCTGCCCTCGCAG	2402
Sbjct	2341	TGTTGTTAGACGACGGGACCGAGGCAGGTCCCCTAGAAGAAGAACCTCCCTGCCCTCGCAG	2400
Query	2403	ACGCAGATCTCAATGCCCGCGTCAGAAGAGATCTCAATCTCGGAATCTCAATGTTAGTA	2462
Sbjct	2401	ACGCAGATCTCAATGCCCGCGTCAGAAGAGATCTCAATCTCGGAATCTCAATGTTAGTA	2460
Query	2463	TTCTTGGACTCATAGGTGGAAACTTACGGGGTTATTCCCTCTACAGTACCTATCT	2522
Sbjct	2461	TTCTTGGACTCATAGGTGGAAACTTACGGGGTTATTCCCTCTACAGTACCTATCT	2520
Query	2523	TTAATCCTGAATGGCAAACCTCCTCTTCTAAGATTACAAGAGGACATTATA	2582
Sbjct	2521	TTAATCCTGAATGGCAAACCTCCTCTTCTAAGATTACAAGAGGACATTATA	2580
Query	2583	ATAGGTGTCAACAATTGTGGGCCTCTCACTGTAAATGAAAAGAGAAGATTGAAATTAA	2642
Sbjct	2581	ATAGGTGTCAACAATTGTGGGCCTCTCACTGTAAATGAAAAGAGAAGATTGAAATTAA	2640
Query	2643	TTATGCCTGCTAGATTCTATCCTACCCACACTAAATATTGCCCTAGACAAAGGAATTAA	2702
Sbjct	2641	TTATGCCTGCTAGATTCTATCCTACCCACACTAAATATTGCCCTAGACAAAGGAATTAA	2700
Query	2703	AACCTTATTATCCAGATCAGGTAGTTAATCATTACTTCAAACCAACAGACATTATTACATA	2762
Sbjct	2701	AACCTTATTATCCAGATCAGGTAGTTAATCATTACTTCAAACCAACAGACATTATTACATA	2760
Query	2763	CTCTTGGAAAGGCTGGTATTCTATATAAGAGGGAAACACACGTAGCGCATCTTGCG	2822
Sbjct	2761	CTCTTGGAAAGGCTGGTATTCTATATAAGAGGGAAACACACGTAGCGCATCTTGCG	2820
Query	2823	GGTCACCATATTCTGGAAACAAGAGCTACAGCATTGCAAAGGCATGGGACGAATCTT	2882
Sbjct	2821	GGTCACCATATTCTGGAAACAAGAGCTACAGCATTGCAAAGGCATGGGACGAATCTT	2880
Query	2883	TCTGTTCCCAACCCCTCTGGGATTCTTCCCGATCATCAGTTGGACCCCTGCATTGGAGCC	2942
Sbjct	2881	TCTGTTCCCAACCCCTCTGGGATTCTTCCCGATCATCAGTTGGACCCCTGCATTGGAGCC	2940
Query	2943	AACTCAACAAATCCAGATTGGGACTTCAACCCATCAAGGACCACTGGCCAGCAGCCAAC	3002
Sbjct	2941	AACTCAACAAATCCAGATTGGGACTTCAACCCATCAAGGACCACTGGCCAGCAGCCAAC	3000
Query	3003	CAGGTAGGAGTGGGAGCATTGGGCCAGGGCTCACCCCTCCACACGGCGGTATTTGGGG	3062
Sbjct	3001	CAGGTAGGAGTGGGAGCATTGGGCCAGGGCTCACCCCTCCACACGGCGGTATTTGGGG	3060
Query	3063	TGGAGCCCTCAGGCTCAGGGCATATTGACCACTGGTCAACAATTCCCTCCCTGCCTCC	3122
Sbjct	3061	TGGAGCCCTCAGGCTCAGGGCATATTGACCACTGGTCAACAATTCCCTCCCTGCCTCC	3120
Query	3123	ACCAATCGGCAGTCAGGAAGGCAGCCTACTCCCATCTCCACCTCTAAGAGACAGTCAT	3182
Sbjct	3121	ACCAATCGGCAGTCAGGAAGGCAGCCTACTCCCATCTCCACCTCTAAGAGACAGTCAT	3180
Query	3183	CCTCAGGCCATGCAGTGG 3200	
Sbjct	3181	CCTCAGGCCATGCAGTGG 3198	